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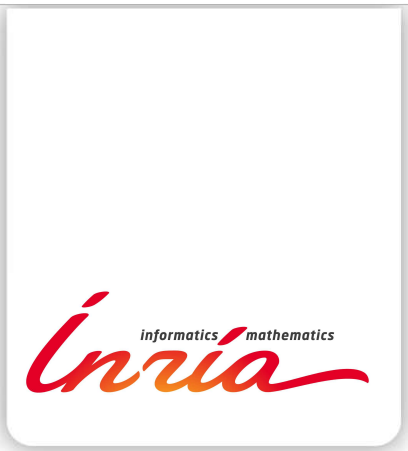
RESEARCH REPORT
N° 7003
september 2013
Project-Teams Carmen

ISSN 0249-6399 ISRN INRIA/RR--7003--FR+ENG



Numerical Investigation in the usefulness of Proper Orthogonal Decomposition method in cardiac electrophysiology

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Research Report n° 7003 — september 2013 — 17 pages

Abstract: Numerical simulation of cardiac electrophysiology is very time consuming. Reduced order method have been recently used in different fields including cardiac electrophysiology. In this paper we use a reduced order method based on the proper orthogonal decomposition (POD), and we propose to evaluate the accuracy of this method while changing different parameters in the model. To describe the propagation of the action potential in the myocardium, we use the monodomain model which is a reaction diffusion PDE system coupled to a dynamic system of ODEs representing the time evolution of the electrophysiology in the cell membrane. We build the reduced order model using a set of parameters, afterwards, we evaluate the accuracy of the reduced model while changing the parameters of the model. We numerically analyze the sensitivity of the reduced order method to the model parameters including the change of the whole ionic model.

Key-words: monodomain model, reduced order method, POD, mitchell schaeffer model, ionic parameters.

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Résumé : La simulation numérique de l'électrophysiologie cardiaque est très couteuse en termes de calcul. Les méthodes d'ordre réduit ont été récemment utilisé dans différents domaines y compris l'électrophysiologie cardiaque. Dans cet article, nous utilisons une méthode d'ordre réduit basée sur la décomposition orthogonale aux valeurs propres (POD), et nous proposons d'évaluer la précision de cette méthode tout en changeant des différents paramètres dans le modèle. Pour décrire la propagation du potentiel d'action au niveau du myocarde, on utilise le modèle monodomaine qui est un système de reaction -diffusion PDE couplée à un système d'équations différentielles dynamique représentant l'évolution temporelle de l'électrophysiologie dans la membrane cellulaire. Nous construisons le modèle d'ordre réduit l'aide un ensemble de paramètres, par la suite, on évalue la précision du modèle réduit tout en modifiant les paramètres de modèle. Nous étudions numériquement la sensibilité de la méthode d'orde réduit par rapport les paramètres du modèle, y compris le changement de l'ensemble du modèle ionique.

Mots-clés : modèle monodomaine , méthode de reduction de modèle, POD, modèle de mitchell schaeffer, paramètres ionique

1 Introduction

In order to make the numerical simulation of electric activity of the heart useable in clinical applications, we need to develop a model that takes into account the physiological properties of the heart and provides realistic propagation of the electrical wave and especially not too expensive in terms of computation cost.

The electrical wave in the heart is governed by a system of reaction diffusion equations called bidomain model, it is coupled to an ODE system representative the cellular activity.

This model, which consists of a reaction diffusion non linear system, is coupled to dynamic system modelling the cellular ionic currents. It is alsoknown to be very expensive from a computation point of view [14, 6]. In this work, we choose the monodomain model [5, 7], a simplified version of the bidomain model, we reduce the complexity of its discretization using a Galerkin basis that apriori contains sufficient informations about the expected solution. There are different methods to construct this basis. Following, [1, 2], we choose to use the Proper Orthogonal Decomposition (POD) method. This approach has been used in many fields of science and engineering, including in parameter estimation for cardiac electrophysiology [1]. But to the best of our knowledge, no work has been done in analyzing the accuracy of this method with respect to changing the parameters of the model. In this work we propose to address the problem of the sensitivity of POD with respect to parameter changing.

The POD is a method to derive reduced models by projecting the system onto subspaces spanned by a basis of elements that contains the main features of the expected solution. This method essentially provides an orthonormal basis for representing the given data in a certain least squares optimal sense. Truncation of the optimal basis provides a way to find optimal lower dimensional approximations of the given data. To be able to use POD in parameter estimation like in [1], we think that a prior study should tackle the sensitivity of the POD solution with respect to the parameters that we want to estimate. Of course, we have a rigorous quantification of the error when the POD method is used to solve the problem with the same parameter with which the POD basis has been constructed. But we don't have any a priori estimation of the error while changing parameters, especially the parameters of the ionic model.

The numerical study that we will address in this work compares the POD solution to the full finite element solution of the monodomain problem when we change the parameters of the ionic model. Moreover, we also check the sensitivity of the method while changing the whole ionic model. In section 2, we will present the mathematical models and the reduced-order method we will be using in this work. In section 3 we will carry out numerical simulation studying the sensitivity of the POD method. The main conclusions of the study are then summarized in section 4.

2 Modelling and numerical methods

2.1 Electric model

The bidomain model is based on the assumption that, at the cell scale, the cardiac tissue can be viewed as partitioned into two ohmic conducting media, separated by the cell membrane: intracellular, made of the cardiac cells, and extracellular which represents the space between them (see [9, 10, 13, 15]). After an homogenization process (see [10]), the intra- and extracellular domains can be supposed to occupy the whole heart volume Ω_H. The heart is assumed to be isolated, the propagation of the electric wave in the myocardium is then described by the following system of equations:

$$\begin{cases} \chi_m \dfrac{\partial V_m}{\partial t} + I_{ion}(V_m, w) - div(\sigma_i \nabla V_m) - div(\sigma_i \nabla u_e) = I_{app} & \text{in } \Omega_H \times (0,T) \\ -div((\sigma_i + \sigma_e)\nabla u_e) - div(\sigma_i \nabla V_m) = 0 & \text{in } \Omega_H \times (0,T) \\ \dfrac{\partial w}{\partial t} + G(V_m, w) = 0 & \text{in } \Omega_H \times (0,T) \\ \sigma_i \nabla V_m . n = 0 & \text{on } \Sigma. \\ \sigma_e \nabla u_e . n = 0 & \text{on } \Sigma, \end{cases} \tag{1}$$

where Ω_H and Σ denote respectively the heart domain and its boundary. The time domain is given by $[0,T]$. And χ_m the membrane capacitance per area unit. The variables V_m and u_e denote the action potential and the extracellular potential, σ_i and σ_e the intra- and extracellular conductivity tensors. The term I_{app} is a given source current, used in particular to initiate the activation, and $I_{ion}(V_m, w)$ represents the ionic current across the membrane. In this study we use the monodomain model [11], where we assume that the ratios of the anisotropy of the electrical conductivity tensor are the same in the intra and extracellular media. Following [5], the reaction-diffusion equation governing the action potential reads as follow:

$$\begin{cases} \chi_m \dfrac{\partial V_m}{\partial t} + I_{ion}(V_m, w) - div(\sigma \nabla V_m) = I_{app} & \text{in } \Omega_H \times (0,T) \\ \dfrac{\partial w}{\partial t} + G(V_m, w) = 0 & \text{in } \Omega_H \times (0,T) \\ \sigma \nabla V_m . n = 0 & \text{on } \Sigma, \end{cases} \tag{2}$$

where $\sigma \overset{def}{=} \sigma_i(\sigma_i + \sigma_e)^{-1}\sigma_e$ is the bulk conductivity.

2.2 Numerical methods

In order to solve numerically the monodomain model, we use finite element method. After discretizing (2) in time, we start by writing the variational formulation of the

problem

$$\begin{cases} w^{n+1} = w^n - \delta t G(V_m^n, w^{n+1}) & \text{in } \Omega_H \\ \chi_m \int_{\Omega_H} V_m^{n+1}\psi + \delta t \int_{\Omega_H} \sigma \nabla V_m^{n+1} \nabla \psi = \chi_m \int_{\Omega_H} V_m^n \psi \\ \qquad\qquad + \delta t \int_{\Omega_H} (I_{app}^{n+1} - I_{ion}(V_m^n, w^{n+1}))\psi & \forall\ \psi \in H^n(\Omega_H) \end{cases} \tag{3}$$

Projecting the variational formulation on the discretized finite element space, we obtain the following linear system

$$\begin{cases} w^{n+1} = w^n - \delta t G(V_m^n, w^{n+1}) & \text{in } \Omega_H \\ \chi_m M V_m^{n+1} + \delta t S V_m^{n+1} = \chi_m M V_m^n + \delta t M (I_{app}^{n+1} - I_{ion}(V_m^n, w^{n+1})) \end{cases} \tag{4}$$

where

$$M = (\int_{\Omega_H} e_i e_j)_{i,j=1,\cdots,n}\,, \qquad S = (\int_{\Omega_H} \sigma \nabla e_i \nabla e_j)_{i,j=1,\cdots,n}$$

and $(e_i)_{1\leq i\leq n}$ is the Galerkin finite element basis. The matrix M is the mass matrix and S is the stiffness matrix. These functions $I_{ion}(V_m, w)$, $G(V_m, w)$ depends on the used ionic model. In this study, the dynamics of w and I_{ion} are described by different ionic models including a two-variables model phenomenological by Mitchell and Schaeffer [8], a four-variables model by Bueno [4] and a complete physiological cell membrane ionic model by TenTusscher [16].

2.3 Reduced order method

For the sake of completeness, we briefly recall the principle of the proper orthogonal decomposition method. The POD is a linear process that includes determining an optimal orthogonal basis of eigen modes in the sense of energy. This means that no base is also capable of capturing a higher amount of energy with the same number of modes. There are two phases in this method, the first is the generation of a reduced order basis and the second is solving the reduced order problem.

2.3.1 Generation of the reduced order basis

The problem to be solved can be stated as follows: how to approximate a function $u(x,t)$ as follows

$$u(x,t) \simeq \sum_{k=1}^{K} a_k(t)\Phi_k(x) \tag{5}$$

where $(\Phi_k)_{k=1}^K$ is a new basis and $(a_k(t))_{k=1}^K$ is a temporal coefficients. Therefore, we need to find the new basis $(\Phi_k)_{k=1}^K$ and the temporal coefficients $(a_k(t))_{k=1}^K$. Assume that we know the values of the function u in m locations $x_1, x_2, \cdots, x_m$ in different p moments.

Let's denote A, the snapshot matrix containing the values of the function u, where each colonne correspond to a given time:

$$A = \begin{pmatrix} u(x_1,t_1) & u(x_1,t_2) & . & . & u(x_1,t_p) \\ u(x_2,t_1) & u(x_2,t_2) & . & . & u(x_2,t_p) \\ . & . & & . & . \\ . & . & & . & . \\ . & . & & . & . \\ u(x_m,t_1) & u(x_m,t_2) & . & . & u(x_m,t_p) \end{pmatrix} \in \mathbb{R}^{m\times p}$$

Solving the problem of approximation (5) is then equivalent to determining the orthonormal basis $\Phi_k(x)_{k=1}^K$ with $K \leq p$ solution of the problem

$$\min_{(\Phi_k)_{k=1}^K \in mathbbR^m} \sum_{i=1}^p \|u(x,t_i) - \sum_{k=1}^K (u(x,t_i),\Phi_k(x))\Phi_k(x)\|^2. \tag{6}$$

The solution of the minimization problem (6) is given by the truncated Singular Value Decomposition (SVD) in the order K of the snapshots matrix A. We refer the reader interested in more details to [12, 18] for a detailed explanation of the link between SVD and POD. Using SVD we obtain,

$$A = U\Sigma V^T$$

where U and V correspond respectively to the the left singular vectors of A of dimension $m \times m$ and the right singular vectors of A of dimension $p \times p$. and Σ is a diagonal matrix containing the $\sigma_1, \sigma_2, \cdots, \sigma_r$, called the singular values of A (and A^T) such as $\sigma_1 \geqslant \sigma_1, \cdots, \geqslant \sigma_r$ with $r = min(m,p)$.

The solution of (6) is given by the left singular vectors of A truncated to order K: we find the matrix Φ as the K first columns of the matrix U

$$\Phi = U_K \in \mathbb{R}^{m\times K} \tag{7}$$

The accuracy of the POD method is related to the following energy quantification [18]:

$$\sum_{j=1}^{p} \|A_j - \sum_{i=1}^{K} (A_i^T \Phi_i)\ \ \Phi_i\|^2 = \sum_{i=K+1}^{d} \lambda_i$$

where A_j is the jth colonne of the matrix A and d the rank.

The number K of eigen modes is choosen such that $\sum_{i=K+1}^{d} \lambda_i$ is less than some tolerance.

2.3.2 Solving the reduced order problem

The POD basis is used by applying a projection procedure, Instead of being projected on the full finite element basis, the variational formulation (3) would now be projected on the POD basis $\Phi = (\phi_k)_{k=1}^K$. Knowing the reduced order solution V_{pod}^n at time t_n,

we look for $V_{pod}^{n+1} = \sum_{k=1}^{K} v_k^{n+1} \phi_k$. The unknown vector $\mathbf{v}^{n+1} = ({v^{n+1}}_k)_{k=1}^{K}$ is obtained by solving the following reduced order problem,

$$\Phi^T(\chi_m M + \delta t S)\Phi \mathbf{v}^{n+1} = \Phi^T(\chi_m M V_{pod}^n + \delta t M(I_{app}^{n+1} - I_{ion}(V_{pod}^n, w^{n+1}))) \quad (8)$$

The left hand side matrix $\Phi^T(\chi_m M + \delta t S)\Phi$ is the reduced order matrix and could be easily inverted once for all in our problem. The right hand side is the finite element right hand-side vector projected on the POD basis.

For both equations, the finite element system (4) and the reduced order (8), we use the *LU* method to determine the full finite element and the POD solutions. In the first case, the order of the matrix $\chi_m M + \delta t S$ is 1681, then it requires 3.166710^9 floating point operations, while the second requires only 3.376910^4. This improvement in the number of operations will be illustrated in the following subsection 2.4, when we will present a comparison of the solutions obtained.

2.4 Numerical comparison between the full finite element and the POD solutions

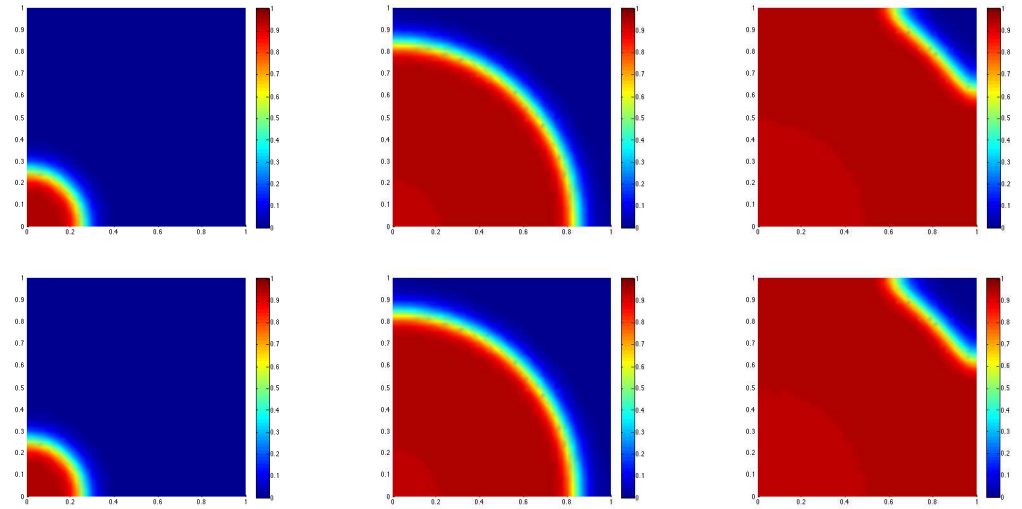
In this section, we present numerical simulations about the POD approximation of the monodomain model. For the sake of simplicity and reproducibility, the heart domain is the square $\Omega_H = [0,1] \times [0,1]$ and the unit is cm. It is discretized on the x and y-axis with a space step 0.025 cm. The time domain is $[0, 500]$, its unit is ms and the time step is 0.5 ms. The heart is stimulated in a region at the left bottom corner $[0, 0.025] \times [0, 0.025]$ during 2 ms. The parameter of the ionic model are given in Table 1.

τ_{close}	τ_{open}	τ_{out}	τ_{in}	V_{gate}
150	120	6	0.3	0.13

Table 1: Original cell membrane parameters.

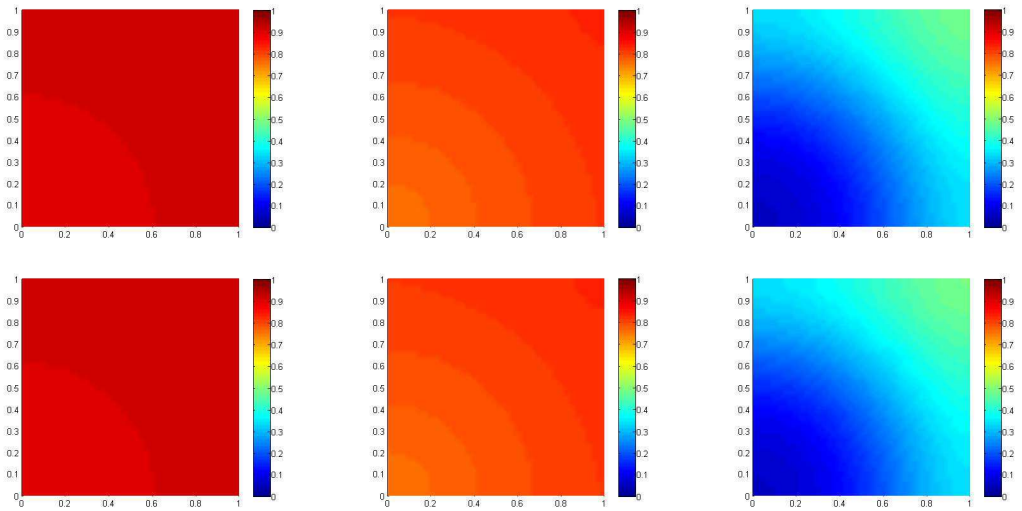
As mentioned in the previous section we start by generating a solution of the monodomain problem. This solution is stored in the snapshot matrix used to construct the POD basis. In this example we have 1681 degrees of freedom. Capturing 99.99 % the finite element solution energy requires only 37 modes. We use these 37 modes as a basis and we solve the POD problem.

Using a matlab code, the full finite element solution costs 10.34 s, where the ODE system costs 0.31 s and the linear system costs 10.03 s. The solution of the reduced order problem is computed in 0.5 s, where 0.31 for the ODE system and 0.19 s for the linear system. In Figure 1, we show three snapshots of the full finite element solution (top) and the POD solution (bottom) at the depolarization phase, and in the Figure 2 at the repolarization phase. The pattern of the solution is the same and the wave front is accurately captured.



Time = 10 ms Time = 30 ms Time = 40 ms

Figure 1: Top (respectively, bottom):Snapshots of the full finite element (respectively POD) solution at times 10, 30 and 40 ms (from left to right) at the depolarization phase



Time = 100 ms Time = 200 ms Time = 300 ms

Figure 2: Top (respectively, bottom):Snapshots of the full finite element (respectively POD) solution at times 100, 200 and 300 ms (from left to right) at the repolarization phase

3 Numerical results

For a given set of parameters and using the standard finite element method, we can compute the action potential and then construct the snapshots matrix A. Using SVD method described above we obtain a reduced order basis that is able to generate the solution up to the considered tolerence. The problem comes when we change some parameters and we try to solve the monodomain problem using the same reduced order basis. Our concern is how the solution of the monodomain problem will behave when using the POD method? What is the accuracy of the method? To answer to these question, we propose to change some parameters in the ionic model and assess the error between the POD and the full finite element solutions. In the paragraph 3.1, we propose to perform this assessment on a phenomenological ionic model with 5 parameters [8] and on a physiological model with a large number of parameters [16]. In paragraph 3.3, we propose to vary the whole ionic model and test if the POD method with a basis computed using Micheall Shaeffer model is able reproduce the solution of Ten Tusscher model.

3.1 Sensitivity of the POD solution to Micheall Shaeffer model parameters

In this paragraph, we use the Micheall and Shaeffer model to describe the electrical activity of the cell membrane. This model is used to describe the phenomenon of excitability while keeping a low complexity, and with only two state variables: the action potential V_m and a recovery variable w. The dynamics of w and I_{ion} are given by:

$$I_{ion}(V_m, w) = \frac{w}{\tau_{in}} V_m^2 (V_m - 1) - \frac{V_m}{\tau_{out}}$$

$$G(V_m, w) = \begin{cases} \dfrac{w-1}{\tau_{open}} & \text{if } V_m \leqslant v_{gate} \\ \dfrac{w}{\tau_{close}} & \text{if } V_m > v_{gate} \end{cases} \tag{9}$$

The time constants τ_{in}, τ_{out} are respectively related to the length of the depolarization and repolarization periods, τ_{open} and τ_{close} are the characteristic times of gate opening and closing respectively and v_{gate} corresponds to the change-over voltage. Using the method of constant variation, we can easily determine the analytical expression of the solution in the interval $[t_n, t_{n+1}]$. For a given time $t \in [t_n, t_{n+1}]$ we have

- if $V_m(t_n) \leqslant v_{gate}$,

$$w(t_{n+1}) = 1 - (1 - w(t_n)) e^{(t-t_n)/\tau_{open}} .$$

- if $V_m(t_n) > v_{gate}$,

$$w(t_{n+1}) = w(t_n) e^{(t-t_n)/\tau_{open}} .$$

The original values of these parameters are given in Table 1 ([8]).

In order to test the accuracy of the POD solution, we first compute the POD basis using the original parameters of the model. Then we propose to perform for each parameter some simulation, where the considered parameter vary between half and three halfs its original value given in Table 1. In table 2, we provide the different considered values for each parameter. We evaluate the error between the reduced order solution and the full finite element solution. All of these simulations are performed in the time domain $T = 500\ ms$ with a discretization step $dt = 0.5\ ms$.

τ_{close}	τ_{open}	τ_{out}	τ_{in}
75	60	3	0.15
100	80	4	0.2
125	100	5	0.25
150	120	6	0.3
175	140	7	0.35
200	160	8	0.4
225	180	9	0.45

Table 2: Parameters used for POD simulations.

In Figure 3, we show the evolution of the L^2 relative errors with respect to parameters τ_{close} (top left), τ_{open} (top right), τ_{out} (bottom left) and τ_{in} (bottom right). For parameters τ_{close}, τ_{open} and τ_{out} the relative error is less than 1%. However, for parameter τ_{in} the error significantly increases when the parameter is far from its original value. In particular for τ_{in} less than 0.175 the error is higher than 1% and it reaches 10% for $\tau_{in} = 0.15$. This means that POD basis constructed with the original parameters is able to approximate the solution with a good accuracy for different values of parameters τ_{close}, τ_{open} and τ_{out}. But for τ_{in}, the accuracy is acceptable (less than 1%) when $\tau_{in} \in [0.175, 0.45]$.

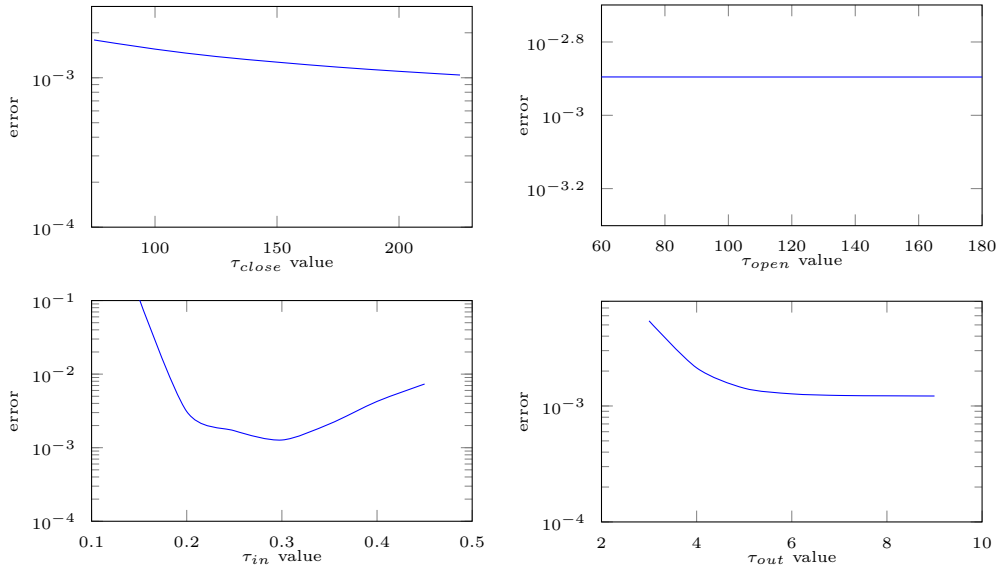


Figure 3: The error between the finite element solution and the POD solution with respect to τ_{close} (top left), τ_{open} (top right), τ_{out} (bottom left) and τ_{in} (bottom right)

In Figure 4, we show the time course of the L^2 relative error between the finite element solution to a POD solution computed for $\tau_{in} = 0,45$. The magnitude of the error is more important in the depolarization phase. In the plateau phase the error is very low but is increases with repolarization phase.

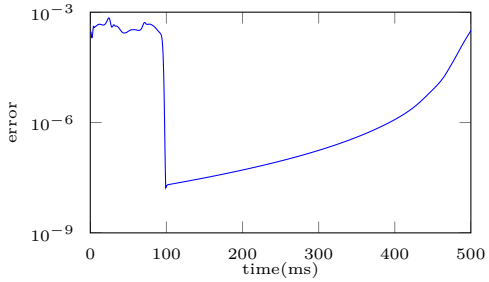


Figure 4: The time course of the spacial L^2 relative error between the finite element solution to a POD solution computed for $\tau_{in} = 0,45$.

3.2 Physiological model

In this paragraph we perform a same study as for Micheall-Shaeffer model but with physiological model Ten Tusscher [16]. The Ten Tusscher Model represents a physiological model of cardiac cell human ventricular. It is established from experimental measurements on the most major ionic currents, and it includes a dynamic basis for calcium. it shows that the differences in the morphologies can be explained by certain characteristics of two currents, potassium current transient outward and slow delayed rectifier, which differ from one type to another cell. The model is described by a set of

differential equations (see [17]). In particular we are interested in evaluating the POD solution to these parameters [16]:

• g_{Na}: the maximal Fast sodium (Na^+) current I_{Na} conductance (the original parameter is 14.838).

• g_{kr}: the maximal rapid delayed rectifier potassium current I_{Kr} conductance (the original parameter is 0.153).

• g_{to}: the maximal transient outward current I_{to} conductance (the original parameter is 0.294).

We compute the space and time L^2 relative error between the full finite element and the POD solutions for the parameters given in Table 3.

g_{Na}	g_{Kr}	g_{to}
7.4190	0.0765	0.1470
9.8920	0.1020	0.1960
12.3650	0.1275	0.2450
14.8380	0.1530	0.2940
17.3110	0.1785	0.3430
19.7840	0.2040	0.3920
22.2570	0.2295	0.4410

Table 3: Cell membrane parameters.

In Figure 5 we see that for g_{Kr} and g_{to}, the solution is suffitiently accurate. However, the parameter g_{Na} the error is low small when the parameter is close to the original value but it dramatticalt increases when the parameter is so far.

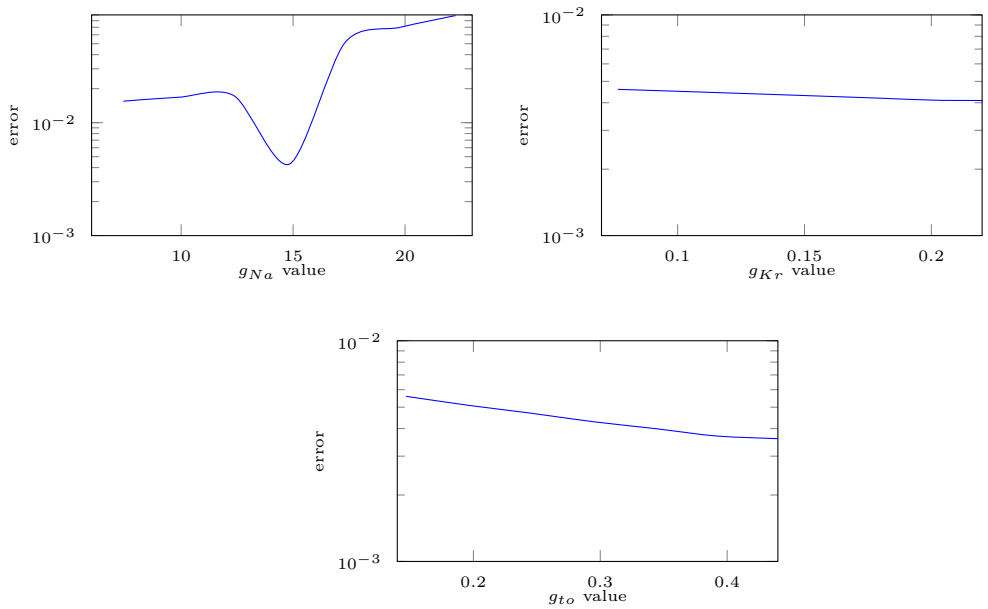


Figure 5: Left (respectively right, bottom) the error between the finite elements solution and the POD solution with respect to g_{Na} (respectively g_{Kr}, g_{to})

3.3 Sensitivity of the POD solution to different models

In this paragraph, we will test the capability of a POD basis constructed using a phenological model (Micheall-Shaeffer) to capture the propagation of the electrical wave governed by a physiological ionic model. Firstly, we generate a finite element solution using the Micheall-Shaeffer model, from this solution we construct a POD basis. After that, we solve the reduced order problem of the monodomain equation coupled to the Ten Tusscher ionic model. We then compute the L^2 relative error between this solution and the full finite element solution of mondomain coupled to Ten Tusscher model. In Figure 6 (left), we plot the time course of this error. We observe that the error is high, mainly at the depolarisation phase where it reaches 10%. We performed the same test for the Bueno et al. model [4, 3]. In Figure 6 (right), we remark that the error is about 1% for this case. These results show that the scale of the action potential values plays an important role. In fact, the action potential values in the Micheall-Shaeffer model are between 0 mV and 1 mV, whereas they are between -86 mV and 25 mV in the Ten Tusscher model and between 0 mV and 1.4 mV in the Bueno et al. model.

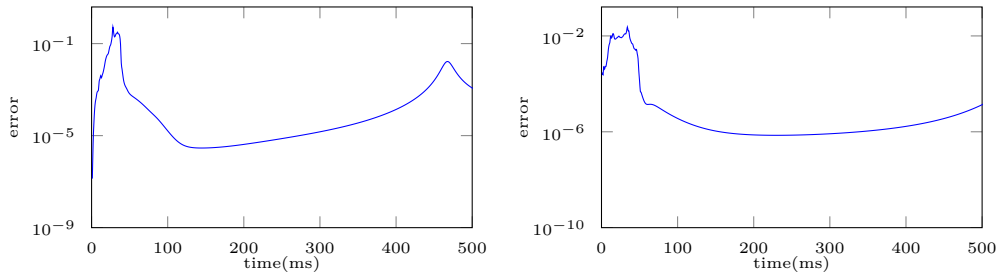


Figure 6: Left (respectively, right), the error between the Micheall Shaeffer full finite element solution and the POD solution of the monodomain equation coupled to the Ten Tusscher (respectively, Bueno) ionic model

For this reason we propose to rescale the Micheall-Shaeffer action potential to the new model before generating the POD basis. In Figure 7 (left (respectively right)), we plot the relative error between the reduced order solution using the new POD basis constructed from data rescaled to Ten Tusscher (respectively, Bueno) model and the full finite element solution. We see in both plots that changing the scale before generating the POD basis improves the accuracy of the solution.

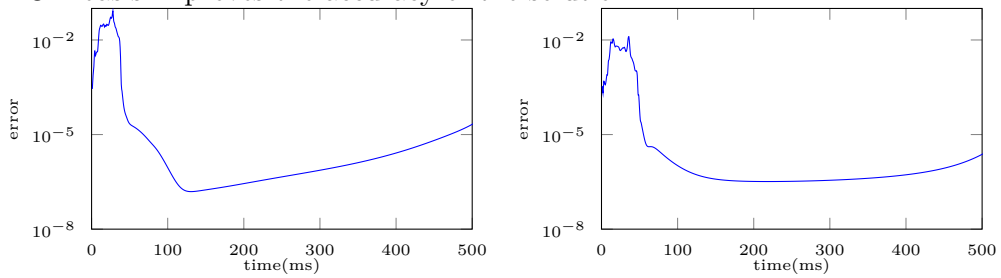


Figure 7: Left (respectively, right), the error between the full finite element solution and the POD solution with scaleted Ten Tusscher (respectively, Bueno) POD basis

4 Discussion and conclusions

We have presented in this work a reduced order approach based on POD method for the computation of the electrical activity of the heart. This approach not expensive in terms of computational cost and is very accurate when we reproduce the solution on which we have build the POD basis. In order to evaluate the usefulness of this approach in parameter estimation problem, we build a POD basis using the original parameters of the ionic model and we computed the L^2 relative error between the finite elements solution and the reduced order solution for different parameters. For M-S ionic model we conclude that we obtain a good accuracy when we vary the values of τ_{open}, τ_{close} and τ_{out}. Whereas for the parameter τ_{in}, we have seen that there is a trust interval, out of it the solution is not sufficiently accurate. For the physiological Ten Tusscher and Panfilov model we have seen that the error between POD solution and the full finite elements solution is acceptable for parameters g_{kr} and g_{to} and important for parameter g_{Na} out of a trust interval. Both parameters τ_{in} for M-S and g_{Na} for the Ten Tusscher and Panfilov

model play an important role in the depolarization phase and the wave front velocity. This explains the sensitivity of the POD solution to these parameters. In order to obtain a good accuracy out of the trust interval, one should update the POD basis.

Since the propagation of the electrical wave has the same pattern if we only change the ionic model, we have tested the case when we use a basis generated from M-S model to solve the Monodomain problem coupled to other ionic models (Ten Tusscher and Pafilov, Bueno). We observed that the POD solution is computed with a good accuracy for the Bueno model. On the contrary, the error is very important for the Ten Tusscher and Panfilov model. We found that this unaccuracy is due to the difference in scale between the transmembrane potential range in different models. Rescaling the transmembrane potential before generating the POD basis comes with an improve of the POD solution mainly for the Ten Tusscher and Panfilov model where the range of the action potential is considerably higher than for M-S model. In future works, we aim to use the POD approach in the parameters estimation problem in cardiac electrophysiology. In particular, we will use physiological optical mapping measurements in order to personalize the electrical model on wedge preparation of animal tissue.

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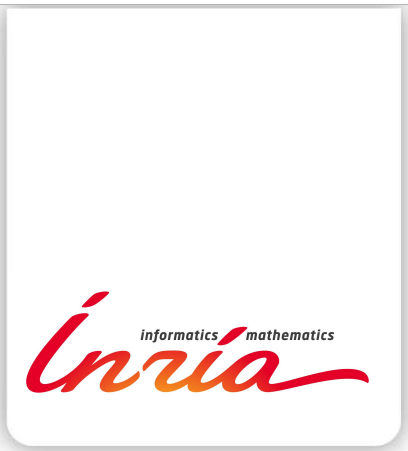

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ISSN 0249-6399